

REMARKS

On August 10, 2006, Applicants timely filed a response to a final office action, and an Advisory Action was issued on August 23, 2006. In this Advisory Action, the Examiner indicates that claims 119-132, as amended on August 10, 2006, are allowable.

With this response, Applicants resubmit claims 119-132 exactly as they were presented on August 10, 2006, and thank the Examiner for indicating that these claims are allowable. Support for, and remarks relating to, amended claims 119-132 can be found, and are incorporated herein by reference, in Applicants August 10, 2006 response.

Also with this response, claims 144-170, and 172-173 are canceled without prejudice, claim 171 is amended, and new claims 174 -178 are presented. Claim 171 has been amended to mirror the claim language found allowable in claim 119. Support for the amendment to claim 171 can be found in the specification at page 23, line 23 to page 24, line 2, and at page 50, lines 14-16, as well as in the Sequence Listing at pages 1 and 5. Support for newly added claims 174 -178 can be found throughout the specification, specifically at page 9, lines 23-24 (mutations include substitutions, insertions, and deletions), and in original claims 4-5 (the mutation inactivates a proteolytic cleavage site).

Like claim 119, claim 171 is directed to a GDF-8 propeptide that has been modified at the aspartate residue corresponding to Asp 76 of SEQ ID NO:5. Unlike claim 119, claim 171 specifies that the GDF-8 propeptide sequence is selected from a

list of non-human GDF-8 propeptides (rather than being at least 95% identical to SEQ ID NO:5). Each of the recited non-human GDF-8 propeptide sequences were known to those of skill in the art at the time of filing and are described adequately in the specification (see, for example, page 7, lines 8-12, page 8, lines 23-25, and page 14, lines 1-4). See also, McPherron et al. (1997) Proc. Natl. Acad. Sci USA 94: 12457-12461, reference attached. Thus, amended claim 171 encompasses fully defined GDF-8 homolog sequences having a mutation that affects only a single amino acid (i.e. at the aspartate residue that corresponds to Asp 76 in SEQ ID NO:5).

Newly added claim 174 is directed to a GDF-8 propeptide that is 95% identical to SEQ ID NO:5, has a mutation at aspartate 76 of SEQ ID NO:5, increases the in vivo or in vitro half life, and inhibits a GDF-8 activity associated with negative regulation of skeletal muscle mass. Thus, this claim falls fully within the scope of allowable claim 119, but differs by reciting a specific GDF-8 activity (activity associated with negative regulation of skeletal muscle mass) that is inhibited by claimed propeptide.

Claim 172 is cancelled, and rewritten as new claims 175-177. Claims 175-177 depend from claim 119, 171, and 174 and further limit those claims by describing the mutation in the GDF-8 propeptide as a substitution, insertion, or deletion. "Mutation" is defined in the specification on page 9, line 23, as including substitutions, insertions, and deletions of amino acids. Thus, new claims 175-177 are fully supported in the application, and do not extend the scope allowable claim 119.

Newly added claim 178 depends from claim 119, 171, and 174, and further limits those claims by stating that the mutation inactivates a proteolytic cleavage site. This amendment is supported in the specification at page 9, lines 24-25, and original claims

4-5. Thus, claim 178 does not extend the scope allowable claim 119, and its entry is requested.

Conclusion

The amendment to claim 171, and the addition of claims 174 -178 do not raise new issues or necessitate the undertaking of any additional search of the art by the Examiner, since all of the elements and their relationships claimed were either earlier claimed or inherent in claim 119 as found allowable by the Examiner. Therefore, this Amendment should allow for immediate action and allowance of the claims as amended.

Accordingly, applicants therefore request the entry of this Amendment, the Examiner's reconsideration and reexamination of the application, and the timely allowance of the pending claims.

Applicants submit that the entry of the amendment would place the application in better form for appeal, should the Examiner dispute the patentability of the pending claims.

Please grant any additional extensions of time required to enter this response and charge any additional required fees to deposit account 06-0916.

Respectfully submitted,

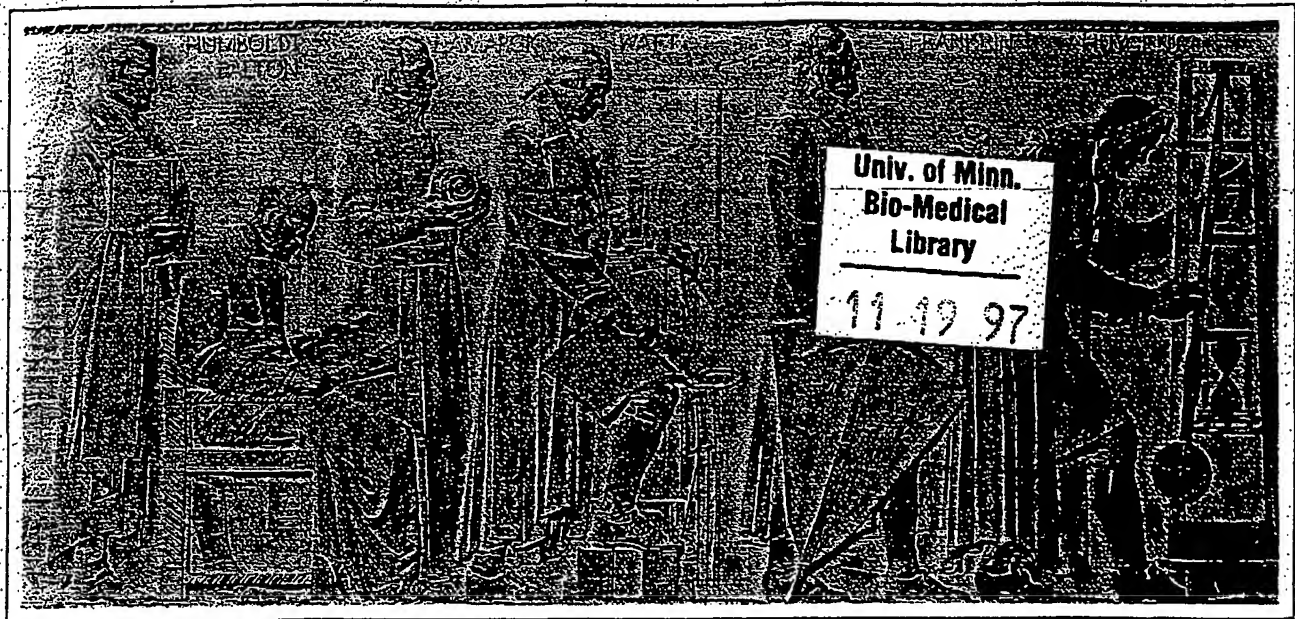
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Double muscling in cattle due to mutations in the myostatin gene

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ABSTRACT Myostatin (GDF-8) is a member of the transforming growth factor β superfamily of secreted growth and differentiation factors that is essential for proper regulation of skeletal muscle mass in mice. Here we report the myostatin sequences of nine other vertebrate species and the identification of mutations in the coding sequence of bovine myostatin in two breeds of double-muscling cattle, Belgian Blue and Piedmontese, which are known to have an increase in muscle mass relative to conventional cattle. The Belgian Blue myostatin sequence contains an 11-nucleotide deletion in the third exon which causes a frameshift that eliminates virtually all of the mature, active region of the molecule. The Piedmontese myostatin sequence contains a missense mutation in exon 3, resulting in a substitution of tyrosine for an invariant cysteine in the mature region of the protein. The similarity in phenotypes of double-muscling cattle and myostatin null mice suggests that myostatin performs the same biological function in these two species and is a potentially useful target for genetic manipulation in other farm animals.

The transforming growth factor β superfamily encompasses a large group of secreted growth and differentiation factors that play important roles in regulating development and tissue homeostasis (1). We have recently described a member of this family, myostatin, that is expressed specifically in developing and adult skeletal muscle and functions as a negative regulator of skeletal muscle mass in mice (2). Myostatin null mice generated by gene targeting show a dramatic and widespread increase in skeletal muscle mass. Individual muscles in myostatin null mice weigh 2- to 3-fold more than those of wild-type mice, primarily due to an increased number of muscle fibers without a corresponding increase in the amount of fat. To pursue potential therapeutic and agricultural applications of increasing muscle mass by inhibition of myostatin activity, we have been characterizing myostatin in animals other than mice. Here we report that the myostatin gene is highly conserved among vertebrate species and that two breeds of cattle that are characterized by increased muscle mass (double muscling), Belgian Blue (3) and Piedmontese (4), have mutations in the myostatin coding sequence. These results demonstrate that the function of myostatin has been highly conserved among vertebrates.

METHODS

Cloning of Myostatin. Poly(A)-containing RNA was isolated from human (obtained from the International Institute for the Advancement of Medicine, Exton, PA), Holstein cow, sheep (Ruppersberger and Sons, Baltimore), pig (Bullock's Country Meats, Westminster, MD), White Leghorn chicken (Truslow Farms, Chestertown, MD), turkey (kindly provided by D. Boyer and D. Miller, Wampler Foods, Oxford, PA) and

zebrafish (kindly provided by S. Fisher and M. Halpern, Carnegie Institution of Washington) skeletal muscle tissue as described (5). cDNA libraries were constructed in the λ ZAP II vector (Stratagene) according to the instructions provided by the manufacturer and screened without amplification. Rat and baboon skeletal muscle cDNA libraries and a bovine (Holstein) genomic library were purchased from Stratagene. Library screening and analysis of clones were carried out as described (5), except that the final washes were carried out in 25 mM sodium phosphate (pH 8.5), 0.5 M NaCl, 2 mM EDTA, and 0.5% SDS at 65°C.

Mapping. Fluorescence *in situ* hybridization was performed on human metaphase spreads (Bios, New Haven, CT) using a digoxigenin-labeled human genomic myostatin probe.

Sequencing of Bovine Genomic DNA. Blood from cattle was spun at $3,400 \times g$ for 15 min, resuspended in 150 mM NaCl and 100 mM EDTA, and digested with 200 $\mu\text{g}\cdot\text{ml}^{-1}$ proteinase K and 1% SDS at 44°C. Semen (Select Sires, Rocky Mount, VA) was digested in 50 mM Tris (pH 8.0), 20 mM EDTA, 1% sarcosyl, 0.2 M 2-mercaptoethanol, and 200 $\mu\text{g}\cdot\text{ml}^{-1}$ proteinase K. DNAs were purified on a CsCl gradient. Exons were amplified by PCR from 1 μg genomic DNA using primer pairs 133ACM 5'-CGCGGATCCTTTGGCTTGGCGTTGCTCAAAGC-3' and 134ACM 5'-CGCGGATCCTTCTCATGAACACTAGAACAGCAG-3' (exon 1), 135ACM 5'-CGCGGATCCGATTGATATGGAGGTGTTTCGTTTCG-3' and 136ACM 5'-CGCGGATCCGGAAGTGGTAGT-TATTTTCACT-3' (exon 2), and 137ACM 5'-CGCGGATCCGAGTAGGAGAGTGTTTTGGGATC-3' and 138ACM 5'-CGCGGATCCACAGTTTCAAAATTTGTTGAGGGG-3' (exon 3) at 94°C for 1 min, 52°C for 2 min, and 72°C for 2 min for 40 cycles. PCR products were digested with *Bam*HI, subcloned into pBluescript, and sequenced.

Southern Blot Analysis of Mutant Sequences. One-fifth of exon 3 amplification products were electrophoresed on 2% agarose gels, blotted to nylon membranes, hybridized with ^{32}P -labeled 13-mers as described (6), and washed in 30 mM sodium citrate, 300 mM NaCl, and 0.1% SDS. Primers used were 146 ACM 5'-ATGAACACTCCAC-3' (Holstein wild-type sequence, nucleotides 936-948), 145ACM 5'-TTGTGACAGAATC-3' (Belgian Blue mutation, nucleotides 931-936 with 948-954), 673SIL 5'-GAGAATGTGAATT-3' (Holstein wild-type sequence, nucleotides 1050-1062), and 674SIL 5'-GAGAATATGAATT-3' (Piedmontese mutation, G1056A).

RESULTS AND DISCUSSION

To clone the myostatin gene from other species, cDNA libraries were constructed from RNA isolated from skeletal

Data deposition: The sequences reported in this paper have been deposited in the GenBank database [baboon (accession no. AF019619), bovine (accession no. AF019620), chicken (accession no. AF019621), ovine (accession no. AF019622), porcine (accession no. AF019623), rat (accession no. AF019624), turkey (accession no. AF019625), zebrafish (accession no. AF019626), and human (accession no. AF019627)].

A commentary on this article begins on page 12249.

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muscle tissue and screened with a mouse myostatin probe corresponding to the conserved C-terminal region, which is mature, active portion of the molecule. An alignment of the predicted amino acid sequences of murine, rat, human, baboon, bovine, porcine, ovine, chicken, turkey, and zebrafish myostatin, deduced from nucleotide sequence analysis of full-length cDNA clones, is shown in Fig. 1. All of these sequences contain a putative signal sequence for secretion and a putative RXXR proteolytic processing site (amino acids 263–266) followed by a region containing the conserved C-terminal cysteine residues found in all transforming growth factor β family members (1). As seen from this alignment, myostatin is highly conserved across species. In fact, the sequences of murine, rat, human, porcine, chicken, and turkey myostatin are 100% identical in the C-terminal region following the putative proteolytic processing site, and baboon, bovine, and ovine myostatin contain only one to three amino acid differences in the mature protein. Zebrafish myostatin is considerably more diverged and is only 88% identical to the others in this region.

The high degree of sequence conservation of myostatin across species suggests that the function of myostatin has also been conserved. To determine whether myostatin plays a role in regulating muscle mass in animals other than mice, we investigated the possibility that mutations in the myostatin gene might account for the increased muscle mass observed in double-muscling breeds. Double muscling, which has been observed in many breeds of cattle for the past 190 years, appears to be inherited as a single major autosomal locus with several modifiers of phenotypic expression, resulting in incomplete penetrance (7). In the most extensively studied double-

muscling breed of cattle, Belgian Blue, the double-muscling phenotype (Fig. 2) segregates as a single genetic locus designated muscular hypertrophy (*mh*) (8). The *mh* mutation, which is partially recessive, causes an average increase in muscle mass of 20–25%, a decrease in mass of most other organs (9, 10), and a decrease in intramuscular fat and connective tissue (11). The *mh* locus is tightly linked to markers on a region of bovine chromosome 2 (12) that is syntenic to a region of human chromosome 2 (2q32) (13) to which we had mapped the human myostatin gene by fluorescence *in situ* hybridization (data not shown).

The similarities in phenotype between the myostatin null mice and the Belgian Blue cattle breed and the similar map positions of the myostatin gene and the *mh* locus suggested the bovine homolog of myostatin as a candidate gene for the *mh* locus. To determine whether the bovine myostatin gene is mutated in the Belgian Blue breed, all three exons of the gene from the full-blood Belgian Blue bull shown in Fig. 2 were amplified by PCR, subcloned, and sequenced. The Belgian Blue myostatin coding sequence was identical to the Holstein sequence except for a deletion of nucleotides 937–947 in the third exon (Fig. 3). This 11-nucleotide deletion causes a frame-shift which is predicted to result in a truncated protein that terminates 14 codons downstream of the site of the mutation. The deletion is expected to be a null mutation because it occurs after only the first 7 amino acids of the C-terminal region, resulting in a loss of 102 amino acids (amino acids 274–375). This mutation is similar to the targeted mutation in myostatin null mice in which the entire region encoding the mature protein was deleted (2). By Southern blot analysis, using oligonucleotides corresponding to the wild-type

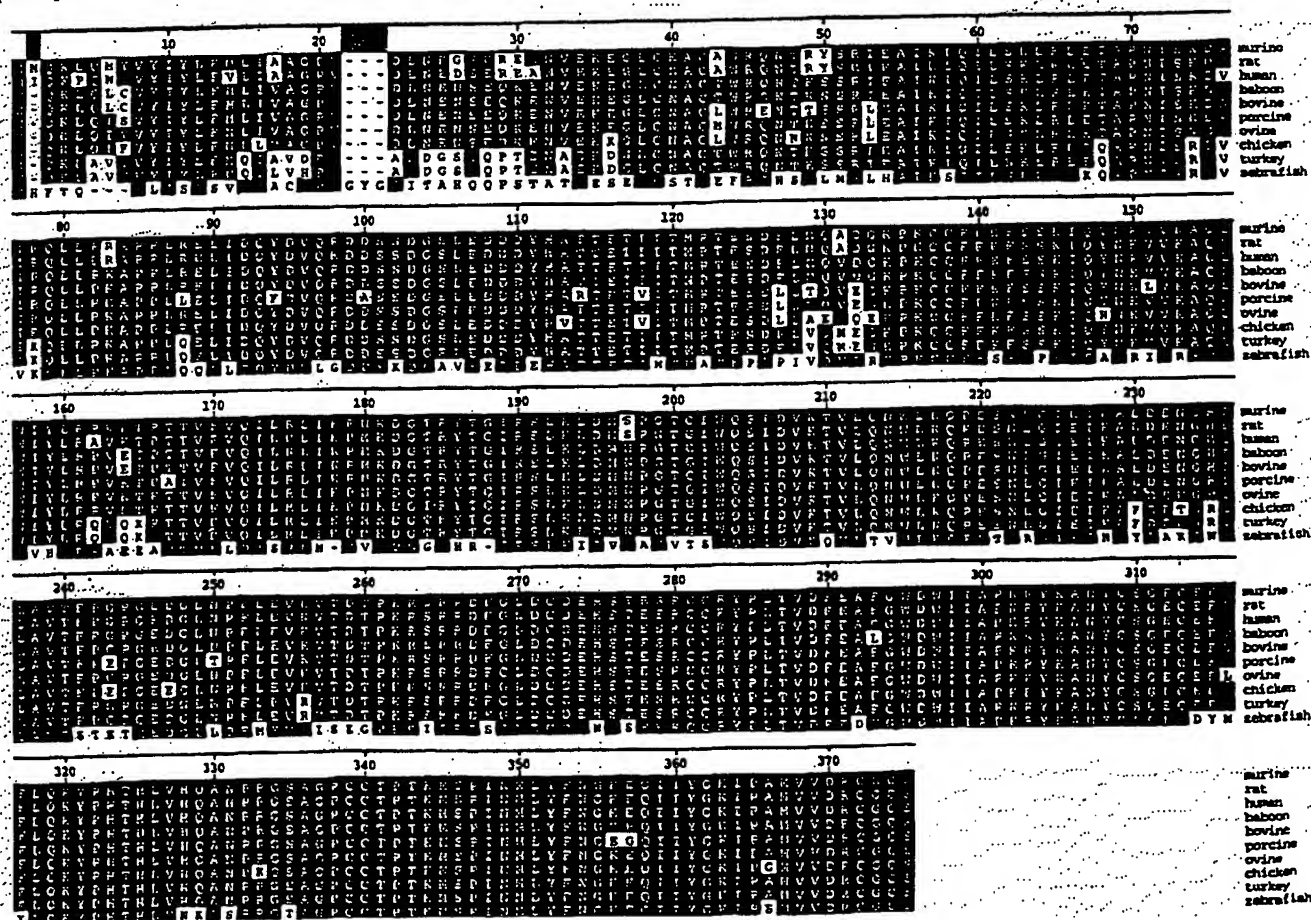
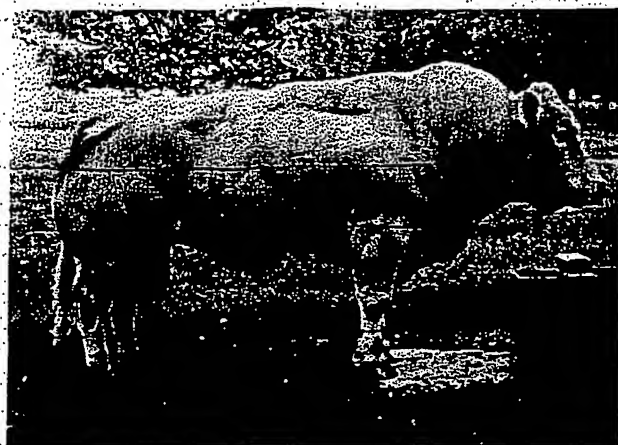


FIG. 1. Amino acid sequence alignment of murine, rat, human, baboon, bovine, porcine, ovine, chicken, turkey, and zebrafish myostatin. Shaded residues indicate amino acids matching the consensus. Amino acids are numbered relative to the human sequence. Dashed lines indicate gaps.



or mutant sequence, this mutation was found in both alleles in 14/14 fullblood Belgian Blue cattle examined (data not shown).

a conservative substitution of leucine for phenylalanine (amino acid 94). The second was a G to A transition in exon 3, resulting in a cysteine to tyrosine substitution in the mature region of the protein (amino acid 313) (Fig. 3). By Southern blot analysis, this mutation was found in both alleles in 10/10, double-muscled Piedmontese cattle examined. This mutation is likely to result in a complete or almost complete loss of function, as this cysteine residue is invariant not only among all myostatin sequences but also among all known members of the transforming growth factor β superfamily (1). This cysteine residue is known to be one of the amino acids involved in forming the intramolecular cysteine knot structure in members of this superfamily for which the three-dimensional structure is known (14-17). Furthermore, when the corresponding cysteine in activin A (cysteine-44) was mutated to alanine, the mutant protein had only 2% of wild-type receptor binding and biological activity (18).

The similar map positions of the myostatin gene and the *mh* locus and the identification of relatively severe mutations in the myostatin gene of two different double-muscled cattle breeds suggest that these mutations are responsible for the double muscling phenotype. To further support this hypothesis, we analyzed DNA isolated from 120 individual fullblood or purebred cattle in 16 other breeds that are not classified as double-muscled (11 Angus, 11 Charolais, 10 Holstein, 10 Brown Swiss, 10 Polled Hereford, 10 Gelbvieh, 9 Simmental, 9 Jersey, 9 Guernsey, 9 Ayrshire, 7 Limousin, 4 Brahman, 4 Polled Shorthorn, 4 Red Angus, 2 Chianina, and 1 Texas

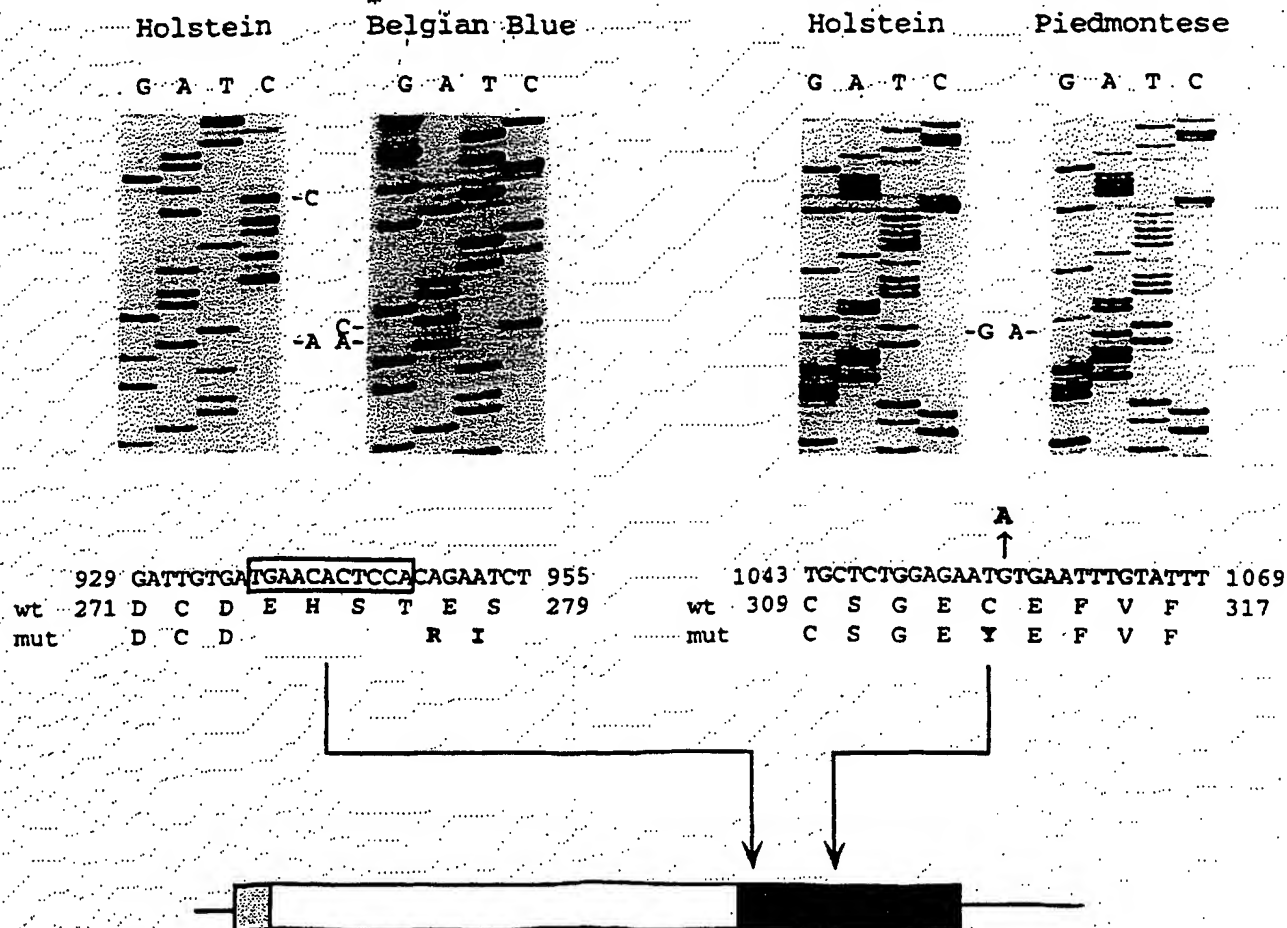


FIG. 3. Myostatin mutations in Belgian Blue (*Left*) and Piedmontese (*Right*) cattle compared with wild-type Holstein cattle. The nucleotides immediately preceding (A936) and following (C948) the Belgian Blue 11-nucleotide deletion are marked. Nucleotide and amino acid sequences are given below and numbered relative to wild type. The Belgian Blue 11-nucleotide deletion (A937-947) is boxed, and the Piedmontese G1056A transition is marked. Bold letters indicate nucleotide and amino acid changes. Arrows identify the locations of the mutations in the myostatin coding sequence. Shading indicates the signal sequence (gray), pro region (white) and mature C-terminal region (black).

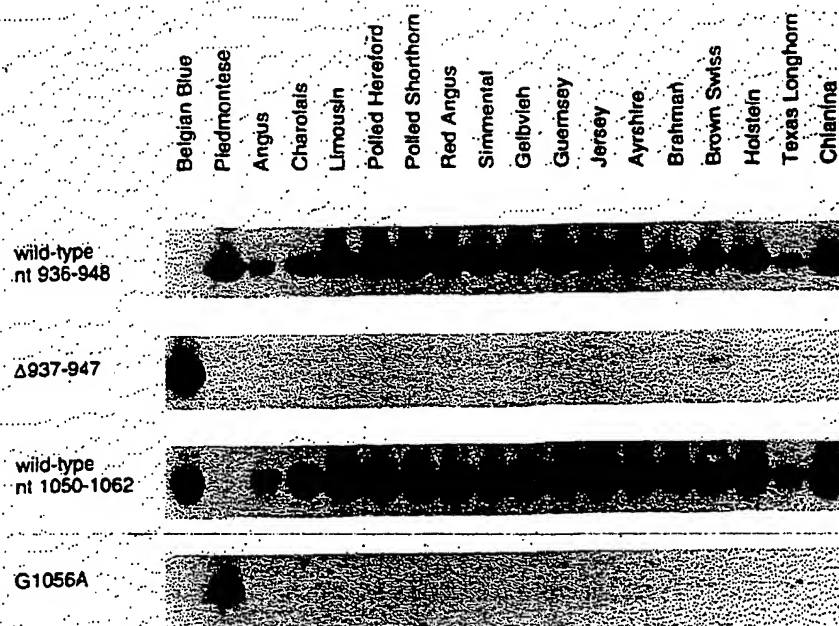


FIG. 4. Representative Southern blot hybridization showing the presence of the Belgian Blue and Piedmontese mutant sequences only in double-muscling breeds of cattle. Exon 3 PCR products were hybridized to oligonucleotide probes spanning the wild-type sequence of the region of the Belgian Blue mutation (top row), the Belgian Blue mutation $\Delta 937-947$ (second row), the wild-type sequence at nucleotide 1,056 (third row), and the Piedmontese mutant sequence at nucleotide 1,056 (bottom row). Differences in band intensity reflect differences in amounts of PCR products loaded, as judged by ethidium bromide staining (data not shown). Homozygosity for the mutations was seen only in double-muscling cattle and not in any conventional cattle as described in the text ($P < 0.001$ by χ^2).

Longhorn) for the presence of each of these mutations (Fig. 4). By Southern blot analysis, the cysteine to tyrosine substitution present in the Piedmontese breed was not detected in any of the 120 individuals. The 11-nucleotide deletion present in the Belgian Blue breed was detected in one allele of a single Red Angus non-double-muscling full-blood bull. In this regard, it has been suggested that the double muscling phenotype that is occasionally seen in many breeds may be due to a single mutation or very few mutations that migrated into many of the European breeds of cattle during the development of the modern breeds (7). Our results demonstrate that myostatin mutations which cause double muscling have occurred at least twice in cattle.

Finally, to rule out the presence of other myostatin mutations in non-double-muscling breeds, we determined the complete sequence of the myostatin coding region of 11 of these breeds (Angus, Charolais, Brown Swiss, Polled Hereford, Gelbvieh, Guernsey, Ayrshire, Limousin, Brahman, Polled Shorthorn, and Texas Longhorn). This analysis revealed only polymorphisms that were either silent changes in the coding sequences or were present in the introns and untranslated regions.

Unlike in mice, a myostatin null mutation in cattle causes a reduction in sizes of internal organs and only a modest increase in muscle mass (20–25% in the Belgian Blue breed as compared with 200–300% in myostatin-deficient mice). It is possible that cattle may be nearer to a maximal limit of muscle size after generations of selective breeding for large muscle mass, unlike mice, which have not been similarly selected. In this regard, even in cattle breeds that are not heavily muscled, the myostatin sequence contains two adjacent nonconservative amino acid differences (EG vs. KE) in the C-terminal region, compared with all other species examined. Although the functional significance of these differences is unknown, it is possible that these two changes represent a partial loss-of-function allele that became fixed in the population during many years of cattle breeding.

For agricultural applications, there are some disadvantages to double-muscling cattle, namely the reduction in female

fertility, lower viability of offspring, and delay in sexual maturation (19). However, in the Belgian Blue breed, the increased muscle mass and increased feed efficiency largely offset these drawbacks (20). The fact that a null mutation in the myostatin gene in cattle results in animals that are still viable and fertile and produce high-quality meat demonstrates the potential value of producing an increase in muscle mass in other meat animals such as sheep, pig, chicken, turkey, and fish by disrupting myostatin function. Indeed, the high degree of sequence conservation in animals ranging from mammals to birds to fish suggests that the biological function of myostatin has been conserved widely throughout the animal kingdom.

We thank Dee Garrels and Chet Pennington (Lakeview Belgian Blue Ranch, Stockton, MO) for providing blood and photographs of Belgian Blue cattle. This work was supported by research grants from the Edward Mallinckrodt, Jr., Foundation and MetaMorphix, Inc. (to S.-J.L.). Under an agreement between MetaMorphix, Inc. and the Johns Hopkins University, the authors are entitled to a share of sales royalty received by the University from MetaMorphix, Inc. The University, A.C.M., and S.-J.L. also own MetaMorphix stock, which is subject to certain restrictions under University policy. S.-J.L. is a consultant to MetaMorphix, Inc. The terms of this arrangement are being managed by the University in accordance with its conflict of interest policies.

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